

PRELIMINARY AMENDMENT ATTACHMENT

8. (Amended) The method according to claim 7₁ wherein the noise profile for each of the other stages is the noise profile for stage 0 scaled by a scaling factor.

9. (Amended) The method according to [clean] claim 8₁ wherein the scaling factor is derived from the end portion of each of the other stages, respectively.

10. (Amended) The method according to claim 5₁ further including applying a threshold to selected stages, the threshold being derived from the noise profile.

11. (Amended) The method according to claim [of] 10₁ wherein the threshold is scaled by a threshold factor before being applied to the selected stages.

12. (Amended) The method according to claim 7₁ wherein the threshold factor is selected so that higher stages of data are filtered less than lower stages.

13. (Amended) The method according to claim 5₁ further including generating a sparse data set indicative of the denoised data.

14. (Amended) The method according to claim 5₁ further including shifting the denoised data to account for variations due to a starting value for the wavelet transformation.

15. (Amended) The method according to claim 1₁ wherein correcting the baseline further includes generating a moving average of the denoised data set.

16. (Amended) The method according to claim 15₁ wherein the moving average is used to find peak sections in the denoised data set.

17. (Amended) The method according to claim 16₁ wherein the peak sections are removed from the denoised data set.

18. (Amended) The method according to claim 17₁ further including generating a baseline correction.

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19. (Amended) The method according to claim 1₁ further including compressing the intermediate data set, the intermediate data set having a plurality of data values associated with respective addresses.

20. (Amended) The method according to claim 19₁ wherein a compressed data value is a real number that includes a whole portion representing the difference between two addresses.

21. (Amended) The method according to claim 19₁ wherein a compressed data value is a real number that includes a decimal portion representing the difference between a maximum value of all the data values and a value at a particular address.

22. (Amended) The method according to claim 1₁ further including performing a mass shift based on the position of the putative peaks.

23. (Amended) The method according to claim 1₁ wherein generating the residual baseline includes deleting an area around each peak in the intermediate data.

24. (Amended) The method according to claim 23₁ wherein the area deleted is derived from a determined width of a peak.

25. (Amended) The method according to claim 23₁ wherein the residual baseline is derived from data remaining in the intermediate data after the peaks have been removed.

26. (Amended) The method according to claim 23₁ wherein generating the residual[.] baseline includes fitting a quartic polynomial to the data remaining in the intermediate data after the peaks have been removed.

27. (Amended) The method according to claim 1₁ wherein the probable peak is located by fitting a Gaussian curve to a peak area in the corrected data set.

28. (Amended) The method according to claim 1₁ wherein the identifying step includes using a generated noise profile to calculate the signal-to-noise ratio for the probable peak.

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29. (Amended) The method according to claim 28₁ wherein a residual peak error is calculated by comparing the probable peak to a Gaussian curve.

30. (Amended) The method according to claim 29₁ wherein the residual peak error is used to adjust the signal-to-noise ratio to generate an adjusted signal-to-noise ratio.

31. (Amended) The method according to claim 1₁ wherein the identifying step includes deriving a peak probability for the probable peak.

32. (Amended) The method according to claim 31₁ wherein the peak probability is derived using the signal-to-noise ratio.

33. (Amended) The method according to claim 31₁ wherein the peak probability is derived by using an allelic [ration]ratio, the allelic ratio being a comparison of two peak heights indicated in the corrected data.

34. (Amended) The method according to claim 1₁ wherein the identifying step includes calculating a peak probability that a probable peak in the corrected data is a peak indicating composition of the biological sample.

35. (Amended) The method according to claim 34₁ wherein peak probability is calculated for each of a plurality of probable peaks in the corrected data.

36. (Amended) The method according to claim 35₁ wherein a highest probability is compared to a second-highest probability to generate a calling ratio.

37. (Amended) The method according to claim 36₁ wherein the calling ratio is used to determine if the composition of the biological sample will be called.

39. (Amended) The system according to claim 38₁ wherein the computer is integral to the instrument.

40. (Amended) A machine readable program operating on a computing device, the computing device being configured to receive a data set indicating composition of a biological sample, the program [implement]implementing the steps of:

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denoising the data set to generate denoised data;
deleting the baseline from the denoised data to generate an
intermediate data set;
defining putative peaks for the biological sample;
using the putative peaks to generate a residual baseline;
removing the residual baseline from the intermediate data set to
generate a corrected data set;
locating, responsive to removing the residual baseline, a probable
peak in the corrected data set; and
identifying, using the located probable peak, the biological sample.